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484 1 Q9955 home sapiers (Funan)
783 1 Q9255 home sapiers (Funan)
725 1 Q1202 home sapiers (Funan)
727 1 F92127 qiardia lamblia (qian
591 1 P28797 cavia porrellus (quin
907 1 P03200 epstein barr Virus (str
3530 1 Q90kn7 home sapiers (human)
                                                                                                                                                                                                                                                          About: Pesulis were produced by the Gengore software, version 4.5,
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                                                                                                                                                                    Copyright (c) 1993-2000 Compugen Ltd.
08-09-527 998A 1 t. Swisspart 39 *
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                                                                   Date: Apr 23, 2002 10:41 PM
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Database sequences: 100059
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Query: US-09-525 998A 1
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SwissProt_39:MY15_HUMAN ·
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1.1 (1941) mus flusculus (fluss 125) pl544 h musch I precurs 1775 (1948) homo saphens (hum 620 | P1398) nicottana tabancum 1589 (P1942) drosophila melano
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Schall LL. Lower M., Roller K.J., Lee A., Hive G.C., Wood G.H.W.,
Getamber T., Gammer G.A., Lentz R., Reab H., Kom W.L., Goeddel D.V.;
"Molecular clouing and expression of a receptor for human numor
pecrosis lactor."
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Neghai V. Prayer C. Rakebasel C. Enjedmann H., LWang K.,
Aderka D. Hoffmann H., Wallach D. Rakebasel C. Enjedmann H., Wallach D.
"Schable forms of time; necrosis forter receptors (NE Es), the cDNA
for the type I INFE, clouded using amino acid neghons class of its
eclable tarm, encodes both the real sails each a soluble form of the
receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Last Sequence update)
20-ATC 2001 (Fel. 17, Last Sequence update)
20-ATC 2001 (Fel. 10, Last Sequence update)
BLOST BROTHER SETEPTOR I PRECURSOR (TUMOR NEGROUS FACTOR BINDING PROFELL 1) (TARA) (TAR-RI) (TAR-RI) (TAR-RI) (CDI20A).
THERSPIA OR THIRL OR THERE.
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Commiss 191019 224(1992).
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#HOLINE Flaventas
Flaventas Francia, Chantry L. Lurner M., Foldman M.;
Floring of Lunnot their Serfests Larlos (TNE) receptor CLNA.
expression of recombinant soluble INF-binding profein.";
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Mammalia, Eutberia, Primates, Catarrhici, Bunilidae, Homo,
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   oi-FFR-1491 (Rel. 17, Created)
      seq_name: SwissProt_39:1NR1_HUMAN
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Swissfritti) Swittelli
Swissfrotti 39:MMCL HUMAN | 1
Swissfrotti 49:MMCL Swissfrotti 39:ENIN TofACC | 1
Swissfrotti 39:ENIN TofACC | 1
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P19438;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the BMB, outstation the European Hoinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed "Isage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lss.bb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF THE ACTO SPHINGOMERINASE.

SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERT LEADS TO HOMOTRIBHERIZATION ONCE ACCREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A ROVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADE, VARIOUS TRADE, INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO THER COMPLEX HY THEIR ASSOCIATION WITH TRADE, THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEASES) MEDIATING APOPTOSIS CONTRIBUTES TO THE INDUCTION OF NONCYTOCIDAL THE EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
                      MEDLINE-90110215; PubMed-2153136;
Engelmann H., Novick D., Wallach D.:
"Two tumor necrosis factor binding proteins purified from human
urine. Evidence for immunological cross-reactivity with cell surface
tumor necrosis factor receptors.";
J. Biol. Chum. 265:1531-1536(1990)
                                                                                                                                                                                                                                                     X-PAY CPYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH THEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLIAR DESCRIPTION.

SUBCELLIAR LOCATION: TYPE I MEMBRANE PROTEIN.

DOMAIN THE FORMIN THAT INDIFFS A SMASE IS PROBARY IDENTICAL TO THE DEATH DOMAIN THE N-SMASE ACTIVATION LOMAIN (NSD) IS BOTH NECESSARY AND SHEPTICHNI FOR ACTIVATION OF N-SMASE.

SIMILARITY: CONTAINS A LA-NGRA/THRR-TYPE CYSTEINE-RICH REGION.

SIMILARITY: CONTAINS I DEATH DOMAIN.

DATABASE: NAME-PROW NOTE-OF GUIDE CALLOR OF THE CALLOR OF
                                                                                                                                                                                                                                                                               MEDLINE-93258809; PubMed-8387891;
Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Naismith J.H., Devine T.Q., Khonó H., Sprang S.R.; "Structures of the extracellular domain of the type I tumor necrosis factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPAPTATE-SPECIFIC CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RESERTOR FOR THE ALPHA THE ALAPTOR MOLECULE FALD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR, THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-PAY OPYSTALLOGRAPHY (1 R5 ANGSTROMS) OF 41-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-97094982; PubMed-8939750;
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AAA61201.1; JOINED.
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CAA01558.1; -.
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191190; -.
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A38208; A38208.
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PIR; A34899; GOHUT1
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TUMOR NECROSIS FACTOR RECEPTOR 1.
TUMOR NECROSIS FACTOR BINDING FROTEIN 1.
                                                                                                                                                                                     Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
3D-structure.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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4CHPHA95D93B8225 CRC64;
                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEATH.
                                                                                                                        PROSITE, PSG0652; TNFR_NGFR_1; 3. PROSITE; PSS0050; TNFR_NGFR_2; 3. PROSITE, PSG0617; DEATH_DOMAIN; 1
                                                                                                                                                                   DEATH_DOMAIN; 1
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InterPro; IPR001368; TNFR_c6.
Pfam, PP00031; death, 1.
Pfam: PF00020; TNFR_c6; 4.
Protom: PD000771; TNFR_c6; 1.
                                                                                 SMART; SM00005; DEATH; 1.
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                                                                                                       SMAKT; SMUU208; TNFR; 4.
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Ratio: 5.466
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0 0	ACTOCLOCAANGGGGAAAGAAAGGGGGAAGGGGAAGTGCTTCTTG [[] [] [] [] [] [] [] [] [] [] [] [] []	350
5.1	PAPATHARAPPARAPAPPAHATRAPPAPPARARAAAAPTARTAPPRAPAPPATAPPARAPPAPPAPPAPPAPPAPPAPPAPPAPPAPPAPPAP	400 134
34	AFFATTGGAGTGAAAAGTHTTGCAGTGCTTCAATTGGAGGGTGTGCTGTGTHTHTHTHTHTHTHTHTHTHTHTHTHTH	450
151	AATGGGACGGTGCACTTTTCTGCAAGAAAAAAAAAAAAA	500 167
01	CIGCCALGCAGGITICITICIAAGAAAACGAGIGIGICICCIGIAGAAACGAACIA 	550
551	ACTGIAAGAAAAACTGTAATGAAGAAA HALGIGTTACOOQASA HGAG HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	500 500
0.1	AATGTWAAGGGAGTGABGALTFAGGGAAGAGAGTGGTGTTGTGGGGGTGGT 	550 217
5.1	CATTITOTITGSDOITIGGGITTATGGGTGGGTGGTGAFDSIIITAATGT 	7.0.0 234
34	ATGGTAGGAGGGGGAAGTGCAAGGGCTGTAGGGCATTGTTGTGGGAAA 	750
51	TCGACACTGAAAAGABBBBACTTGAAGBACTACTACTAAGCCCTTTTTTTTTT	800
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34	OCTITGASICCCGIGCCCACTITCCACTTTCACTTTCAGGGGGGGGGG	300
= =	OPPOGLIGAVIGIODPAAPTI IOPPOPIOCAGAGAGGIGGGAGAGAG 	950 317
951 317	CTATCAGGGGGTGANDOATONT DAGGANADOGTGANDTOGAGNONA 	1 ñ ñ û ĝ 3 3 4
2. 4.	1000CAACCCCTTCAGAAGGGGAGGATAGTGCCACAAATATAGAATTTTTTTT	1656 350
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010	CCCSTTGCGCTcstAnstAnTrostasranorrtAcasarTcAcstAnrand PHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT	1150 384

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between the swiss Institute of Bioinformalies and the EMBL outstation. The European Bioinformatics Institute, There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial of the content is the commercial of send an email to Dicensellsbirth.
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-1- FUNCTION: RECEPTOR FOR TWF-ALPHA. THE ALAPTOR MCLECULE FADD

RECRUIS CASPASE-8 TO THE ACTIVATED PEDEPTOR. THE PERULTING

AGGREGALE CALLED HE DEATH INDOCTING SCHALLES OTHERS.

PERFORMS CASPASE-8 PROTECULING SCHALLES OTHERS THE

CHREGARE OF CASPASE-8 PROTECTION WHICH IN LITES THE

CHREGARES MADIATING AND SCHALLS SHICH OF CYSTHINE

PROTERESES MADIATING AND SCHALLS SHICH OF CYSTHINE

PROTERESES MADIATING TO THE PYTEMPORT OF TRANS OF INPET LEADS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMOTRIMERIZATION, ONCE AUGREGATED THE RECEPTORS DEATH DOMAINS FROVIDE A BOVEL MOLECCLAR INTERFACE THAT INTERACIS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD, VARIOUS IRADDO-INTERACIINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-001-1996 (Rel. 34, Greated)
01-001-1996 (Rel. 34, Last sequence update)
20 A103 2022 (Rel. 49, Last attaclation update)
TUMOR NECESIS FACTOR RECEPTOR 1 PRECURSOR (P60) (INF-RI) (INF-RI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATES A LIAST TWO DISTINCT STONALING CASCADES, APOPTOSIS, NF-KARPA E STONALING (BY SIMILARITY).
SUBSCELLULAR LOCATION: TYPE I HERBRANE PROTEIN.
SIMILARITY: CONTAINS A LANGEKATHER TYPE CYSTEINE KICH REGION.
SIMILARITY: CONTAINS A LANGEKATHER TYPE CYSTEINE KICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukoryota, Metazoa, Chordata, Craniata, Vertekrata, Euteleostomi,
Mammalia, Eutheria, Cetariiodaciyia, Sulna, Suldae, Sus.
                                                                                                                                                                       1201 TACAGCATGUTGH CGACCTGGAAGGGGGGGACGCACGGGGGGGGGGGCCAC 1250
                                                                                                                                                                                                                                                                                                                                          1251 GCTGGAGCTGTTGGGACGCGTGCTCCGCGACATGGACCTGGTGGGCTGGC 1300
1151 AGATEGATEGOGTIGGAGETGCAGAACGGGGGGTGTTTGCGGGGAGTGGGAA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.01 | 19GAGGAMATHGAAGGGGGTT11.GGGGGGGGGGGGGGGHG1.GGGGCGGGGGG | 135.0
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InterPro; IPR001368; INFR_c6

FMRL: 019994; AAC48499.1; -. InterPro; IPROGO488; Death.

LINE

HSSP; P19438;

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Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
SIGNAL 1 21 POTENTAR
                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                            TUMOR NECROSIS FACTOR RECEPTOR 1. PYTRACHILULAR (POTENTIAL).
                                                                                                                                                N-SMASE ACTIVATION DOMAIN (NSD).
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N-LINKED (GIGNAC. ..) (POT
M-CD72361EGG0C9143 CRC64,
                                                                                                 CYTOFLASMIC (POTENTIAL).
                                                                                                                                                              SIMILARITY
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                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                           POTENTIAL.
                                     PROSITE: PSSO050; TNFP NGFR_1: 3. PROSITE: PSSO050; TNFR_NGFR_2: 2. PROSITE: PSSO017; DEATH_DOMAIN: 1.
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3
3
4
              ProDom; PD000771; INFR_c6; 1.
                                                                                                                                                                                                                                                                                    50696 MW,
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6: 3.
                       SMART; SM00005; DEATH; 1.
SMART; SM00208; INFR; 3.
                                                                                                  461 AA;
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TRANSMEM
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REPEAT
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Gaps: 4 Percent Identity: 71,645 Length: Quality: 1738.00 Ratio: 4.526 Bilarity: R3.117 Percent Similarity alignment_scores:

US-09-525-998A-1 x TNR1_PIG aliqument_block

to: 461 from: 1 Align seg 1/1 to: TNR1_PIG

- 17 aLeuLeuValAspValTyrProAlaGlyValHisGlyLeuValLeuHisP 34
- 101 TAGGGGACAGGGGAGAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATC 150
- 201 CHYGHACAAFSACIGIOCACOCOCOCOCACAHACOCACHOCACOCACH 250 rLeuHisAsnAspCysLeuGlyProdlyLeuAspThrAspCysArgGluC 29
- 251 GTGAGAGGGGTCCTFCACGGTFCAGAAAACCACTCAGACACTGGCCTC 300

GRADAGAGGTHAGAGAGAGGTGATGAGGGGGGGGGGGGTGTA 1079 992 OCHANGO MATCHO CAACA COLOUTTO AGAAGTGGGAGGACAGGCCCACAAG 1041 1130 GCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGG 1179 1080 - ddaadiraaridaadaadaraadaada iridaadiradaadaariridaraadaa - 1129 383 401 ATTATTGGAGTGAAAACTIITECAGTGTTGAATGGAGGTGIGCCIC 450 200 ThrArgAsnAspPheGlnAspThrGlyThrThrValLeuLeuProLeuVa 216 701 ATCHTACTACCATGGTGGAAGTCTACTACTCCATGTTTGTGGGAAA 750 . GOGOTHOPPOPOPOPOPOPOPOP 316 eAlaProProProGinGlyAlaGlyProTleLeuProMetProProAlaS 333 151 AATGGGAGGGTGGAGGTGTGGTGGGAGAAAAAAAAAAGGGGTGTGGGAG 500 167 nCysHisSerGlyPhePheLeuArgAspLysGluCysValSerCysValA 184 551 ACTRITAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600 184 snCystysAsnAla...AspCystysAsnLeuCysProAlaThrSerGlu 199 601 AATĞITAAGGGTAÇIGAGGAÇIÇAĞGCAQCAÇINGININININGÇÇÇINGIN 650 651 CATITITICITITICGETETTGCCTTTTATCCCTCCTCTTCATTGCTTAATGT 700 799 GOGGGGGAAAGGATTCAGTGGCACTGCAGGCTTCACCGCCACGC 847 848 IGGGCTTCAGTCCCGTGCCCAGTTCCACCTCACCTCCAGCTCCACCTAT 897 283 hrThrPheSerProValProSerPheSerProlleSerSerProThrPhe 299 300 ThrProCysAspTrpSerAsnIleLysValThrSerProProLysGluIl 316 942 GOCACCACCCTATICAGGGGGCTGACCCCATCCTTGCGACAGCCCTCGGCT 991 501 CHGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 266 rPhcClyprollcThrPhrPheScrProllcProScrPhcScrPhcThrT NOT AGCTIG/TH/CCAAAHGCCGAAAAGGAAAHGGGT/CAGGT/GCAGAHGT/CTT/CTT/G 350 AlaHisSeiAlaPioAlaGluLeuAlaAspAlaAspProAlaThrLeuTy 151 CACACHOGAPOGGGACACOTIGTIGGTAGGAAGAACCAGTAGGGG 751 TCGACACCIGAAAAAGAGGGGAGCITGAAGGAACTACTACTAAGCCC... 898 ACCCCCCCCCACTGCCCAACTGC

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use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an equies a license agreement (See http://www.isb-sib.ch/announce/or send an equal to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### Himmler A., Maurer-Footy I., Kromke M., Scheurich P., Pfizenmaier K., Additon A., Maurer-Footy I., Kromke M., Stratowa C., Adolf G.R.;

### Himmler A., Maurer-Footy I., Kromke M., Stratowa C., Adolf G.R.;

### Molecular clouing and expression of human and rat tumor necrosis

### Tactor receptor chain (p60) and its soluble derivative, tumor

### DAM Cell Balo., 9776-715(190).

### Charling Protein.";

### Charling Protein.";

### Charling Reference For The ACTIVATED RECEPTOR. THE RESULTING

### CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING

### CASPASE-8 TO THE ACTIVATED WHICH INITIATES THE

### CASPASE-8 TO THE ACTIVATION WHICH INITIATES THE

### SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE

### PROTEASES) MEDIATING TO THE EXTRACELLULAR DOMAIN OF INFRI LEADS TO

### CHARLING TO THE EXTRACELLULAR DOMAIN OF THEN DAMAINS

### PROTEINS SUCH AS TERSEY BY NOW POSSIMIY FARD. ARE PECPUTED TO

### INFRI COMPLEX BY THEIR ASSOCIATION WITH TARD. THIS COMPLEX

### CACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

### CACTIVATED COMPLEX BY THE ASSOCIATION WITH TARD.

### CACTIVATED CASPASES OF THE OFFICE OFFICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ratius norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Kodentia; Sciurognathi; Muridae, Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Pel. 40, Fast annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-P1) (TNF-R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS A LA-MEFEVTUPE (YSTEINF-HICH MEGLON).
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
1280 ACATGSACCTGCTGCTGCTGCTGCTGGASSACALGGASGAGGAGGAGTTTGCGGC 1329
                                                                                                                                                                                    1230 PATRITING GRIGGERAGE TANDAT GRADITALI GRADA DA 16010 DE 1279
                                               1330 CCCGCCCCCCCCCCCCCCCCCAGTCTTCTCAGA 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 ProAlaArgLeuAlaProAlaProHisLeuLeuArg 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91090841; PubMed-1702293;
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Interpro: IPR001368; INFR_c6.
Pfam: PF00531; death: 1.
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PIR; B3655; B36555.
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P22934:
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Receptor, Transmembrane, Glycoprotein, Repeat, Signal, Apoptosis,
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                       TUMOR MEDROSIS FAUTOR RECEPTOR 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                            N-SMASE ACTIVALION DOMAIN (NSD)
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CYTOPLASMIC (PHIENTIAL).
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FRESILE: FRS0050, INFR_NGFR_2: 3.
PROSITE: PS50017: DEATH_DOMAIN: 1.
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Probom, PD000771; INFR_c6; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; INFR; 3.
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US-09-525-998A-1 x TNR1_KAT
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Percent Similarity:
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|227| GPGPAPGPPGPPGPSPSAGSPPAPSPFGGAGCFGPFGGAGGAGGAGGFGGFGGFGG

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980 CAGCCCTCCCCTCCCACCCCATCCCAACCCCTTCAGAAGTGGGAGGAC 1029
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                                            351 CACAGTGGACCGGGAAACATGTGTGACTGCAGGAAGAACAACTAGTAGTGGC 400
                                                                                                                                            134 rqTyrLeuSerGluThrHisPheGlnCysValAspCysSerProCysPhe 150
                                                                                                                                                                                                                                               151 AsnGlyThrValThrileProCystysSlutysSlnAshThrValCysAs 167
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                                                                      801 GGCCCCAAAC......CCAAGCIICAGTGCCAGTGCAGGTICAGGTTGCAGA
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Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
"Molecular cloning and expression of the mouse Inf receptor type b.";
Immunogenetics 34:338-340(1991).
                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rcl. 22, Created)
1 MAY 1992 (Rcl. 22, Last sequence update)
20-MDR-2001 (Pp.) 40, Last annotation update)
TUMOR NECKOSIS PACTOR RECEPTOR 1 PRECURSOR (Pr0) (TNF-PI) (TNF-PI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodwin R.G., Anderson D., Jerry B., Davis T., Brannan C.I., Copeland N.G., Jonkins N.A., Smith C.A., Molecular Cloning and expression of the type I and type 2 murine receptors for tumor necrosis factor.";
Mol. Cell. Biol. 11:3020-3026(1991).
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Gray P.W., Feldmann M., Fowell B.M.J.,
"Cloning, expression and cross-linking analysis of the murine p55
Lumor necrosis factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia, Eutheria, Rodentia, Sciuroquathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and expression of cDNAs for two distinct murine tumor nerrosis farior receptors demonstrate one receptor is species
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Bebo R F , Linthicum D S.;
"Nobled De Sequence of the TNE Type I receptor from a mouse
                                                       MEDILINE-91187885; Pubmcd-1849278;
Lowis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
                                                                                        433 ysAspMetAsnLeuArgGlyCysLeuGluAsnIleArgGluThrLeuGlu 449
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                                                                           454 AA
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                                                                                                                                                                                                    seq_name: SwissProt_39:TNR1_MOUSE
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    NF-KAPPA B SIGNALING (BY SIMILARITY).
SUBCELLULAR LOCATION - TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LANSFEINELYEE CYNSTEINE-PICH PESION.
SIMILARITY: CONTAINS I DEATH DOMAIN.
Mol. Immunol. 30:165-175(1993)
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Receptor: Transmembrane: Glycoprotein; Repeat; Signal; Apoptosis POTENTIAL. TUMOR NECROSIS FACTOR RECEPTOR 1. N-SMASE ACTIVATION DOMAIN (NSD). EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). SIMILARITY
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TNER-CYS 2.
INFR-CYS 3.
TNFR-CYS 4. POTENTIAL. DEATH. PROSITE: PS00652; TNFR NGFR 1; 3. PROSITE: PS50050; TNFP NGFR 2; 3. PROSITE: PS50017; DEATH_DOMAIN: 1. EMHL, X59238; CAA41922; EMHL, X57796; CAA40936; EMHL, 1,26349; AAA5936; Lirenberg, 1,26349; AAA40465; Lirenberg, M88677; AAA40465; Lirenberge, M76655; AAA40 Interpro: IPPG00488; Death. Interpro: IPR001368; TNFR_c6. Pfam: PF00531; death: 1. Pfam: PF0020; TNFR_c6, 4. Probom: PE000771; TNFR_c6; 1. SMART: SM00005; DEATH: 1. EMBL; M59377; AAA40464.1; -. PIR, S16677, S16677. PIR, S19021, S19021. HSSP, P19438, 1EXT. MGD, MGI:1314884; Infestla. PIR; A38634; COMSTI 443 443 1126 1126 1167 1167 1102 1102 1168 1168 DOMAIN TRANSMEM DOMAIN DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DOMAIN REPEAT REPEAT REPEAT REPEAT DOMAIN DOMAIN SIGNAL CHAIN

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N-LINEED (GECNAC. ..) (F-TENTIAL).

N-LINEED (GLCHAC. ..) (F-TENTIAL).

K-Y-G (IN MFF. ..) (F-TENTIAL).
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Ratio: 4.133 Gaps: 7
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US-09-525-998A-1 x INR1_MoUSE
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  DISULPID
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20-AUG-2001 (Rel. 40, Last annotation update)
TÜMÖK NECKUSIS FACTOR RECEPTOR I PRECURSOR (PGG) (TNE-KI) (TNE-KI)
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 | SerGluValValProThr...GlnGlyAlaAspProLeuLeuTyrGluS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 AlaHis...ProGlnArgProAspAsnAlaAspLeuAlaIleLeuTyrAl 361
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217 uValifeteuleuClyteuCysteuteuSerrheiferheifeSerteum 234
                                                                                                       698 IGIAICGCTACCAACGGIGGAAGICCAAGGICIACIOCALGGIGGG 747
                                                                                                                                                             748 AAATCCACACCTCAAAAAGAGGGGGGGGCTTGAAGGAACTACTACTAAGCC 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPCPCAAAPPPAAGPTFCAGTONIAGTONAGGPTFTCACOT 841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 CystenArgoluAlaGlnTyrSerMetLeuGluAlaTrrArgArgTh 411
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20-ABG-2001 (Pel. 40, East sequ
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformalics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                   PERFORMS CASPASE 9 PROTECTION WHICH INTITATES THE STREET CASPASE (ASPARTATE) WHICH INTITATES THE STREET CASCALE OF CASPASES (ASPARTATE) FREETING CYSTEINE PHOTEASES, MEDIATING ADOPTORS (49° SIMILARITY).

SUBBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERI LEADS TO HOMOTRIMERIZATION ON'T AGGRESSATED THE REPEPTORS DEATH FOMAINS PROVIDE A NOVEL MALEGINAR INTERACT: SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFE, RIP AND POSSIBLY FADD, ARE RECRUITED TO THERI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
                                                                                                                                                                                                                                                                                 ACTIVALES AT LEAST TWO DISTINCT SIGNALING CASCADES, AFORTOSIS AND
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N-LINKED (GLCNAC. ..) (POTENITAL).
N-LINKED (GLCNAC. ..) (POTENITAL).
                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS A LA-NGER/THER TYPE CYSTEINE-PICH PEGION. -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                    "Cloning of cONA encoding bowine tumor necrosis factor-receptor 1
                                                                                             Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

1. FUNTION PEREPT-REPORTED THE ADELTOR MOLECOLE FADD
PERPHITS CASPAGE 9 TO THE ACTIVATED PECEPTOR. THE RESULTING
AMPRIATE FALLED THE DEATH-INGUING STRUBLING COMPLEX (DISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprofein, Repeat; Signal; Apoptosis
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                                                                                                                                                                                                                                                                                               NF-KAPPA B SIGNALING (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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                                        TISSUE-Aorta;
Log E.-K., Talyor M.J., Kehrli M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PSQUESS: TWFR_NGFR_1: 3.
PPOSITE: PSSOUSO: TWFP_NGFP_2: 2.
PROSITE: PSSOUSO: DEATH_DOMAIN: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPROGO488; Death.
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Pfam; PF00020; TNFR_c5; 3.
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SIGNAL 1 21
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CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL). SEQUENCE 471 AA; 51367 MW: 5243LP514DFB81C4 CRC64,
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US-09-525-998A-1 x INRL_BOVIN
                                                                                                                                                                                                          aliqnment_scores:
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7 2	51 TGGACCTGAAAAGAGGGCAGTTICAAGGAACTAT.ACTAAGCCCTTT 	800 261
க் ப்	01 0GCCCCAAATCCAAGGTTCAGTCCCAGTTCTATCCCCACCTGG 1::1	850 274
7 30	51 GCITCAGICCGGGGCCAGILCGACTICACCICS AS ISCA STAIACC HILLI STILLININI STAIL STAIL SA YSPIGSETSCF Dr.ProSetSetProValSetTiCProbrotyClyrice	900 290
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ion in	76 24 erThrHis	187 140
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10.	26 GGACAOCCCCACAAGCCACACCTAGACACTOATGACCGGGGGGGGGGGG	1072
10.	73 CGCIGIAGGCGIGGIGGAAAGGGGCCCCGGGGGAITGCGGGGGGGGGG	1122 890
31.	23 GTGGGGGGTAGGGGTGGAGGAGGAGGALGGALGGAGGGAG	1172 407
111.	73 GAARGONORIOREGOOOGOOOGAALACAGONIGUIGOOOGAGUTTI 1111 1111 1111 1111 1111 1111 1111	222 24
12:	23 GGGGGGCANGGCGGGGGGGGAAGAGCAGGAGGGGGGGGGG	272 49
12.	73 CTCCGGGACATGGACCTGCTGGGGCGCACACACACACGCGCT THE THILL THE THILL THE THILL THE THILL THE THILL THE THILL THILL THE TAX LEGAL ASSISTED AND ACCOUNT ASSISTED AND ACCOUNT ASSISTED AND ACCOUNT ASSISTED AND ACCOUNT ACCO	or .)
13:	323 11GCGCCCCCCCCCCCCCCCCCCCCCCCCCTCTTCT	
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DI 00 6		
7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	0-AUG-2001 (Rel. 40, Last annotation update) SL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DE3) (ADOP EDIATING RECEPTOR TRAME) (DEATH DYMAIN REFERENCE) (WS. PROTEIN	3) (APOPTOSIS
DE C	APOPIOSIS INDUNING RECEPTOR AIR) (APO 3) (IYM-HWAYTE AS RECEPTOR OF DEATH) (LARGO, 100, 30, 30, 30, 30, 30, 30, 30, 30, 30,	SOCIATED
S S S	NESSTIZ OR WELL OR WEL OR APO1 OR DR3 OR DDR4. One Sapiens (Human)	•
25	Ţ	. [110] . (50)

the Swiss Institute of Bioinformatics and the EMBL outstation

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FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-H (NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY PLAY A ROLE IN FEGULATING LYMPHOCYTE HOMEOSTASTS.
SUBDINIT: HOMODIMER. INTERACTS STRONGLY UT THE DEATH DOMAINS WITH THE THIRL ASSOCIATED MOLECULE TRADD AND THE THREE TREEPING TO ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                                                              Geeddel D.V., Giles K.M., Pun K.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T., Hahne M., Schreeter M., Wilson A., French L.E.,
Browning J.L., Macdonald H.R., Tschopp J.,
"TRAMB, a novel apoptosis stediating receptor with sequence homology
to tumor negrosis factor receptor I and Pas(Apo-1/CD95).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND LYMPHOCYTES, DETECTED IN LYMPHOCYTE-RICH LISSUES SUCH AS THYMUS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHROELLILAR LOCATION: TYPE I MEMBRANE PROFEIN (POTENTIAL).
ALTERNATIVE PROPRICTS: 3 ISSOCIATED WIL-17/LAPI-1A (SH'WN HEPE),
WEL-SL/HAPE-3 AND WEL-S2: APE PROFINED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kappa-B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: GLYCOSYLATED (PROBABLE).
SIMILARITY: CONTAINS A LA-NGFR/INFR-TYPE CYSTEINE-FICH FESTION
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97148200; PubMed-8994832;
Marsters S.A. Sheridan T.P. Donahue C.T., Pitti P.M., Gray C.E.
Goddard A.D., Bauer K.D., Ashkenazi A.;
                                                                                                                                                                                                                                                                                                 Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garq M., Duan D.R., Xinq L., Genfr R., Ni J., Dixit V.M.; Signal transduction by DP3, a death domain-containing receptor related to TNPR-1 and CD95.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "LARD: a new lymphoid-specific death domain containing receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin P. Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          Kitson J., Raven T., Jiang Y.-P. Geeddol D V., Giles K M., Pun
Grinham C.J., Brown R., Farrow S.N.;
"A death-domain-centaining reveptor that mediates apoptosis.";
Nature 384:372-375(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLON, INTESTINE, AND SPILEEN, ALSO FOUND IN THE PROSTATE.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97222233 Pubmod Glidora.
Screaton G R , Xu X - N , Olson A.L., Cowper A.E., Tan R.,
McMichael A.J., Hell J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandhary P M , Hood T F.;
Submitted (JAM 1997) to the EMBL/Cenbook/EDBL databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulated by alternative pre-mRNA splicing.";
Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
                                                                                                                                                                                                                                                           TISSUE-Umbilical vein endothelial cells;
                                                                                                      MEDLINE-97088617; PubMcd-8934525,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain, and Fetal lung;
MEDLINE-97205335; Pubmed-9052839;
                                                                                                                                                                                                                                                                             MEDILINE-97081063; PubMcd-8875942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curr. Biol. 6.1669-1676(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 7-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 4-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Science 274:990-992(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF-KAPPA B SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunity 6:79-88(1997).
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                      NCB1_Tax1D=9606;
                                                                                      TISSUE-Lymphoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11SSUE-Heart;
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the European Bioinformatics Institute, There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed Trager by and for commercial entitles requires a license agreement (See http://www.ish-sib-ch/announce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLGPGAPGWPCGPPFAWGHPDLHIPPLLASQAPGYCR (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEWVQVLIJAGLVVPLJLJGATLTYTYRHCWPHKPLVTADEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEAL/PPPATHLS -> SRWCAGNARGRTGMDRGEAGERGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWERL INTERACTION.
P->A SUPPPESSES HOMODIMERIZATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .- >A: SUPPRESSES HOMODIMERIZATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEGSCFEROAAVOGWROMFWWWVLLAGLUVVELLEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L->A: SUPPRESSES HOMODIMERIZATION, FR
INTERACTION, AND APOPTOSIS INDUCTION.
                                                                                                                                                                                                                                                                                                                            Alternative splicing, Transmembrane, Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHPTPTSCFQCSGSRCSWLALWSPSCLGPP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM WSL-S2).
MISSING (IN ISOFORM WSL-S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOFORM WSL-S1).
MISSING (IN ISOFORM WSL-S1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPR -> AAA (IN REF. 6).
P -> H (IN REF. 7).
P -> L (IN REF. 6 AND 7).
A -> R (IN REF. 1).
P -> L (IN PEF. 1).
F -> H (IN PEF. 1).
F -> H (IN PEF. 1).
                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5226319DFDB46706 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \begin{array}{ccc} {\rm Gaps:} & 22 \\ {\rm Percent:identity:} & 28.294 \end{array}
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                                                                                                                                                                                                                                                                                                                                                              WSL-1 PROTEIN.
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                                                       of send an email to licensedish sib.ch).
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TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                              INFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEATH.
                                                                                                                                                                                                                                                                                           PROSITE: PSAA652; INFP_NGFP_1; 2.
PPOSITE: PSSAA6050; TNFP_NGFR_2; 1.
PROSITE, PSSAA17; DEATH_DOMAIN; 1.
                                                                         EMBL, Y09392, CAA70561.1; EMBL, YU9332, CAA70559.1; EMBL, Y09392, CAA70560.1; EMBL, U72763, AAC50819.1; EMBL, U83599, AAB41434.1; EMBL, U74611, AAB41918.1; EMBL, U94504, AAC51309.1; EMBL, U95810, AAC51192.1; EMBL, U95810, AAC51192.1; EMBL, U95810, AAC51192.1; EMBL, U95810, AAC51193.1; EMBL, U83597, AAB41432.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45385 MW;
                                                                                                                                                                                                                                                           1PR001368; TNFR_C6.
                                                                                                                                                                                                                                                IPROOO488; Death
                                                                                                                                                                                                                                                                      Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR c6;
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106
218
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Ratio:
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200
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alignmest_block: US-09-525-998A-

17 TO: WELL_HUMAN ### 17 TO: WELL_HUMAN from: 1 TO: 417 CICCIGGAGGTATGGGAAATATACCCTCAGGGGTTATGGACTGGT LEULEULEUWALLEUWAN FROM: 1 TO: 417 CICCIGGAGGTATGGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAA

no n	33 4011CA-000A20016440111A0100044200A0417.A0011A00 88
7	58AlaHisThYLeuLeuAlaProProAspSerSerSFREST.CCys 272
∞ (ı	83 1CCAddicAddiAlACCOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
о 0	- 30
- O - M	35 GASAGGIGGCACCACCATCAGGGGGCTGACCCATGCGTGCGACAGCC 984
о м	985 CTCGCCTCGACCCCALCCCCATCAGAAGTGGAAGAGCGGGGGGGGGG
10	35 CCACAAGCCACAGACCTACACACTGATGACACACACACAC
10	55 TGGTGGAGAVGTGGGGGTGGGGGGGAAGGAATISSE BSGGGGCTA 1
33.	35 GOGGIGAGGGACGACGGACGGCCGGGCGGGGGGGGGGGGG
. II	85 CCTGCGCGAGGCGAATACAGGAGGCGCGCGGCCCCGGGGGGGG
12	35 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
12	285 GACCTCCTCCCTCGAGGACAFCGAGGACTT 1323
sed_na	name: SwissProt_39:1NKC_HUMAN
Seq_do ID_T AC	ud_documentation_block: TRRC_HUMAN STANDARD: PRT: 435 AA. PAR441:
100	1-JUN-1994 (Rel. 19, Created) 1-JUN-1994 (Rel. 29, Last sequence update)
DE 2	0 AUG 2001 (Ref. 40, Last annotation update) XMPHOLGXIN-BELA RECEPTOR PRECURSOR (LUMER NEGROSIS FACTOR RECEPTOR
GN	RELATED PROTEIN) (TOMOR NECROSIS FACTOR C RECEPTOR). Ibr or infor or indrses.
SS OC E	omo sapiens (Human). ukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
X X	ammalia, Eutheria, Primates, Catarrhini, Rominidae, Homo. CBI_TaxID-9606,
RN RP S	1] EQUENCE FROM N.A.
RC RX M	ISSUE-Liver; FDLINE-93252381; Pubmcd-8486360;
A H	acts M., Chaffatet M., Cassiman Jose, in mergine H., Marynen P.; Construction and evaluation of a biconaly of human 12p
PL S	ranscribed sequences derived from a somatic cell hyprid."; enomics 16:214-218(1993).
N dX	2] UNCITION.
KA KA	EENING 9425529; Dubmed-8171323; Trowe P.D., van Arsdale F.L., Walter H.N., Mare C.F., Hossion C.
RA RT	A lymphotoxia beta specific receptor.";

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-!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGEP/TNEE-TYPE CYSTEINE-EICH MEGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 GCCACTGGTGCTCCTGGAGGTGTTGGTGGAATATATACGCTTCAGGGGTTA 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYMPHOTOXIN-BETA RECEPTOR
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SIGNAL
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BY SIMILARITY
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ProDom; PD000771; TNFR_c6; 1.
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52 uProdinHisArg IleCysCysSerArgCysProProdlyThrTyrV 68
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"A constitutive promoter directs expression of the merve growth factor receptor gene.";
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20-AUG-2001 (Rel. 40, Last annotation apdate)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NAF MECHPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
-1- SIMILARITY: CONTAINS A LA-NGPR/THPR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa: Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarfhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
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NT-3, AND NT-4.
..... 1007
                                                                                                                                                         1007
                                     1022 GOGRAGAMAGGGGGGAGAMAAGGAAAAAGGMAAAAAAGGAAHAAGGGGGGG 1071
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                                                                                                                                                                                                                                                                                                                                                                                      360 ASBITGTYTITGTYTASBGTYPT@ValleuC!yGTyPT@Pt@Clyptg...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 AA
971 ICCTTGGGACAGGCCTGGGCTGGGACGCGALGCGGAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 ... GlyAspLeuProAlaThrProGluProProTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87051725; PubMcd-3022937;
Johnson D. (anahan A.) Buzk C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-22 FROM N.A.
MEDLINE-89096903; Pubmod-2850481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 ProflyProProglyLeuSorFhrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sehgal A., Patil N., Chao M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_39:NGFR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1269 CGIGCICCGCGACAT 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 ArgClyProArgAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GP80-LNGFR) (P75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bothwell M., Chao M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
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                                                                                                                                                                                                                                                                                                           1008 .....
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PO8138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKED (GLGNAC. . .) (POTENTIAL) B09FA14 #PH3D625B GRC64;
                                                                                                                                                                                                                                                                                               LOW ALTINITY NERVE SROWIN FACTOR
                                                                                                                                                                                                                                                             Transmembrane, Glycoprofein: Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 ProArquentententententententsyalScriendiydiyAla.. 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 CCACTORTON OF GGAGCTGTTGTTGGGGAATATAGCCTTCACTGATTAT
                                                                                                                                                                                                                                                                                                                   (1.44 (1.14x) (1.4x)
                                                                                                                                                                                                                                                                                                                            POLINITAL.
CYTOPLASMIC (POLENITAL).
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Percent Identity: 23.819
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N LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                   4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                 INFR CYS 3.
INFR-CYS 4.
-!- SIMILARITY: CANTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                         INFR-CYS 2.
                                                                                                                                                                                                                                                                                                          RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                        DEATH.
                                                                                                                                                                                                                             PROSITE: PSG0652; INFR_NSFR_1; 3. PROSITE: PS50650; INFR_NGFR_2; 4. PROSITE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45183 MW;
                                                                                                                                                            InterPro: IPRO00488; Death.
InterPro: IPR001868; INFR.c6.
                                                                                                       EMBL; M14764; AAB59544.1; -.
                                                                                                                                                                                  Pfam; PF00531; death; 1.
Pfam; PF0070; iNFR_c6; 4.
SMART; SMU0005; DFA1H; i.
SMART; SM00208; INFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-525-998A-1 x NSPR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 240.50
Ratio: 1.108
milarity: 44.559
                                                                                                                                                                                                                                                                          Phosphorylation: Signal.
                                                                                                                                                                                                                                                             Receptor: Neurogenesis;
                                                                                                                                                                                                                                                                                                                   107
1122
1138
1146
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1180
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HSSP; P07174; INGR.
MIM; 162010;
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67
86
83
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                                                                                                                                                                                                                                                                                             CHAIN
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134 33	CCCAAGAAAATATATCTACTCAAAATAATTGGATTTGCTGTACCAAG	183 46
184	TGCCACAAAAGGAACCTACTTGTACAATGACTGTGAGGCCGGGGGGAGGA ::: ::: :::	233 61
234	TACGGACTGCAGGGAGTGTGAGAGGGGCTT 	280 78
281	ACCACCTCAGACACTGCTCAAATGCGAAATGCGAAAAGGAAAATGGGT ::	330 91
331 92	Caddingagarererer LeuginserMetserAlaP	377 108
378 108		427
122 122		4 7 4 138
475 139	CAGGAGAAACAGAACACCGTGTGCACCTGC ::	521 155
522 155	AACACAAAACCACTGTGTGTGTGTTTTTTTTTTT	555 172
556	sp.1	597
598 189		647 193
64 8		697
19.3		193
598 194	TGTATCGCTACCAACGTGGAAGTCCAAGGTCTACTGCAT 	747 198
748	AAATCCACACTOCAAAAAAAGGGGAGCTTGAAGGAACTACTACTAAGGC ::::: :: :: ::	797
798	CCTORCECEAAAQCEAAAC TTGAGEGGACEGGAGGTTGA 	83.8 23.2
339	COCCCAGCCTGGGCTTCWITCCGGGCCASITCGACCTTCACCCCCAGC	888 248
389	TCGACCTATACCCCCGGTGACTGTGCGAAGTTTGCGGGP	927
328	ວວວ	952
ur Si	plouvalalamprilhalambet psaramrpassaerrystyschoason	. A.
353	ATCAGGGGGTGAGGCCATGGTTGAGAGAGAACTGGACTTCCAGA	996

	282 ysGlnGlyAlaAsnSe.	III::: rArgFroValAsnGlnIhr2	93
	997 CCCATCCCCAAGGG	_	040
	294 ProProProGluGly		310
	1041 GCCACAGAGCTAG	GCCAYAGAG CTAGAYACTGAGCCGGGGGGGGGGGGGGGGGGGGGGGGGG	.083
	310 pserdinserLeuHi	~:	12.7
	1084 327 InAlaLeuLysGlyAspGlyG	GTGGTGGGAAGGTGCCCCCGTTGCGC ::: :::::::! ::: lyLeuTyrSerSerLeuProProAlaLys	1110 343
	_		11115
	344 ArgSluGluValGlu		360
	1116 GGAATICGTGCGGC :::::::::::::::::::::::::::::::		1165 375
	1166 ARTGRAMANER		.215
	375 erPheThrHisGlu		388
	1216 APPTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ลาการสลสอกออกออกออกออกออกออกสลอกออกสอบอบออกออกออกออก 	1255 402
	1266 AndrendIdellonand		1315
	402 uAlaAlaLeuArgAn	itti::	415
	1316 AGGCGCTTTGC 1326 ::: 415 luSerLeuCys 418	بو	
sed	_name: SwissProt_39:TNRC_MOUS	NRC_MOUSE	
seq. ID	documentation_block: TNRC_MOUSE STAN	seq_documentation_block: ID TWRC_MOUSE STANDARD; PRT; 415 AA.	
AC	P50284; 01-00T-1996 (Red	4. Created)	
TO	01-OCT-1996 (Rel.	4, Last sequence update)	
DE	LYMPHOTOXIN-BETA RE	os Last annotation update) MEPTOR PRECHRSOR.	
S O S S	LTBR OR TNFCR. Mus musculus (Mouse	. (
င္ ဝ	Eukaryota; Metaroa; Mammalia; Butheria;	Chordata, Craniata, Vertebrata, Butel Rodentia, Sciurograthi, Muridae, Muri	deostomi; inac: Mus.
X 0	NCB1_TaxID=10090;		
N N N	(I) SEQUENCE FROM N.A. STRAIN-CVR. TISSHE-		
젊	MEDLINE-96072804; 1	ubMod-7594541;	·
R R A A	Browning J.L., Ward	R.N., Hessign C., Tizard R., Kozak C.A. (C.E.)	`. ∀
RT	"Mouse lymphotoxin	beta receptor. Molecular genetics, lic	gand binding
RL	J. Immunol. 155:528	0-5288(1995).	
X X	[2] SEQUENCE FROM N.A.		
RX RA	MEDIINE-96163885, I Nakamura I., Tashir	ubmed-8586432; o K., Nazarea M., Nakano T., Sasayama	ŝ
RA	Honjo T.,		
z z	"The murine lymphot sequence trap and c	oxin-beta receptor cona: isolation by hromosomal mapping.";	the signal
ž į.	Genomics 30:312-319	(1995). TOR FOR THE LYMPHOTOXIN-BETA, POSSIBLE	POSSIBLE FUNCTION IN
9 5	IMMUNE DEVELOPM	ENT. ATION TYPE I MEMBRANE PROTEIN.	

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-! SIMILARITY CONTAINS A LA-NAPEZINES-TYPE CYSTEINE FICH FEGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 CCTCAAAATAATTGGATTHGCTGTAGGAGGAGGAAGGAAGGAAGGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuValProProTyr, 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgileGluAsnGlnThrOysTrpAspGlnAspLysGluTyrTyr 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuteuGlyLeuSerGlyLe 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (FOTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor, Transmembrane, Glycoprotein, Repeat, Signal.
SIGNAL, 1 30 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238320A5c6AEF661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. CYTOPLASMIC (POTENTIAL)
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1.220 Gaps: 22
43.132 Lengert Genrity, 26.056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom, PD000771; TNER_c6; 1.
SMART; SMAC208; TNEP; 3.
PPOSITE: PS00652; TNER_NGEL; 2.
PROSITE; PS50060; TNER_NGEL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, U29173; AAA68964.1; -. EMBL, L38423; AAB0846.1; -. EMBL; U30798; AAA81334.1; USSP, P25942; LCDF. MGD, MGD, MGT, TORPTS; IFP. InterPro; IPR001368; INFR_C6. Pfam; PF00020; TNPP_C6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44356 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 uLeuValAlaSerGlnProGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-525-998A-1 x TNPC_MOHSE
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Ratio:
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DISULFID
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507	\TCACTGT@CG@GGGGGGGGAGGAIAC 	8 9 2
r r	riği nAspit	84
254 84	AAAACCACO 	303 100
304	SGTCAGGTC YPheGlu	353 117
354	119CAGGA7 1 ::: JCysClnP1	403 134
134	SCTTCAALU 	
148	CACCICICA AlaGluVal	488 154
489	CCAldCAGO 	529 179
530	GTAAGAAAA ::: SGInProl	579 195
580 194	STIAAGGGG	629 210
510	GTGCT ::::: :QLTALBM.	555
656	ideliei ieA Hissi sabhethrī	705 243
706 244	ACTUALI	755
756	MesaArt1Ac 	805
806 263	SAGGCTTCA Cys	3 2
856		869
	0 TTCCACTICACOLCOMAGINGACOTATACOCCCG	
905 310	31CCCAAC1 	936 326
937		24.2
326	uproclyGluHisClyGlnValAlaHisGlyAlaAsnClyIlCHisValI	34.3
200	F550	100

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between the Swiss Institute of High Connaties and the EMHL outstation the European Bloinformatics Institute There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is no femoved itsage by and for commercial entities requires a license absence (See http://www.isb-sib.ch/announce.or send an email to license@isb sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liepinsh E., Hag L.L., Otting G., Thanez C.F.; "NMR structure of the death domain of the p75 neurotrophin receptor."; EMBO J. 16:4999 5065(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chórdata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93077038; PubMed-1446821; Metsis M., Persson H., Mctsis M., Timmusk T., Allikmers P., Saarma M., Persson H., "Regulatory elements and transcriptional regulation by testosterone and retineing anid of the rat nergo growth factor receptor promoter."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
"Gene transler and molecular cloning of the rat nerve growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988 (Rel. 07, Greated)
1-APR-1988 (Rel. 07, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
1-OW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLUIAR LOCATION: TYPE I MEMPRANE PROTEIN.
1- PTM. N. AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
1- SIMILARITY: CONTAINS A LA-NGFR, TYPE CYSTEINE-PICH PROTION.
1- SIMILARITY: CONTAINS I DEATH DOMAIN.
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                                                                                                                                                                                                         997 CCCATCC...CCAACCCCCTTCACAATTCCACACACGCCCCACAAGCC 1043
                                                                                                                                                                                                                                                 343 hrGlyGlySerValmbrValmhrGlyAsnileTyrileTyrAsnGlyDio 359
                                                                                                               425 AA
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PTP: A26441; A26441.
PHP: 1NGR; 29-JUL-97.
INTOTPTO: IPROBATH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                   PROSITE: PSEGGES: TNFP_NGFR_1; 3.
PROSITE: PSEGGES: TNFF_NGFR_2; 4.
PROSITE: PSEGGES: TNFF_NGFF_20MAIN; 1.
Receptor: Neurogenesis: Transmembrane; Glycoprotein: Repeat;
Phosphorylation; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 GTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACT 89
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Interpro; IPRO01368; TNFR_c6.
                                Pfam; PF00531, death, 1.
Pfam; PF00020; TNFR_c6, 4.
                                                                                                     SMART; SM00005; DEATH; 1. SMART; SM00208; INFR; 3.
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<	IIGGAGCTCTGCCTCAATGGGACCCGI ::: aCysScrvalCysClavalCryScrClyAc	480
< − "I	AACACCORGIOCACCIOCCATOCAGGITTGTTFCT. 	527 158
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	.AAGAAAAGCTGGAGTGCAGAAGTIGTGCCTACCCCAGA :::::: uArgGinLcuArgGluCysThrProTrpAlaAspAlaGluC	603 191
C >	ACTCAGGCAGGAGAGTGC1GFTGGGGGGTGGT	653
-	PCTTTGGTGTGTGTTTATG	174 703
•		194
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~ - F	TGAAAAAGAGGGGGGAGG - -	800 212
_ <u> </u>	GGCCCAAACCTGAGCCTGAGCCTGAGGCTGAGCCTGAGCCGGGCGGG	850
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	1075clgtsdgggggggtggayaacyrgcgggg 1103
	334 GlyAsnLeuTyrSerSerLeuProLeuThrLysArqGlusluValGluLy 456
	1104 GTIG
	1142 GCGNCACAMATCATOSALGGASCICCAAASSOCA ESCIBOS 1191 11 :::::::
	1192 GAGGCGAATACAGCATCHTGGGGACCTGTAUGGGGGAAAGGGGGGGGG 1241 :::
	1242 GGAUSTOTANISTICEGANDERSANDERSHOCKER ANALYSTANCTISC 1291
	1292 IGGGTGCTGGAGGACATCGAGGAGGCGTTTGC 1826
r_pos	name: SwissProt_39:INk2_McUSE
seq_ tD AC	Seq_documentation_block: ID TNR2_MOUSE STANDARD; PRT; 474 AA. AC P25119; P97893:
분통.	01-MAY-1992 (BCL. 22, Created) 01-MAY-1992 (RCL. 22, Last sequence update)
E B :	<pre> Felgh: 999 (RC): 38, Last anotation update) THOR NETPOSTS PATTOR PECEPTOR 2 PRECURSOR (INF-R2) (P75).</pre>
8 S	INFERTS OF THEE 'RET'S. Mus musculus (Mouse).
88	Eukaryota, Wetanba, Cherdata, Craniata, Vertebrata, Enfeleostomi, Ammmalia, Eutheria, Rodentia, Schorognathi, Muridae, Murinae, Mus.
N N	NCB1_(ax (D=10090)
RR	SEQUENCE FROM N.A. MEDLINE-91187885; PubMed-1849278;
K A	lewis M., lattadia L.A., Lee A., Bennett G.L., Rice G.C.,
X X	Mong bill, then this acedael D.V.; "Closing and capitession of cOMAs for two distinct monitor fumor
RT TA	necrosis factor receptors demonstrate one receptor is species
RL	Specific. ; Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
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RA V	Goodwin R.G., Anderson D., Jerzy R., Davis I., Brannan C.I., Coceland N.G., Jenkics N.A., Smith C.A.;
RT	"Molecular cloning and expression of the type 1 and type 2 murine
<u> </u>	receptors for tunor merosis factor;; Mol. Cell. Biol. 11:3020-3026(1991).
R KN	(3) SEQUENCE OF 1 26 FROM N.A.
X	STRAIN-NOD);
RΛ ∷	Jarob C.O., Liu J.: Submittad (CAM 1996) to the eMbs. Dergask Lore, databases.
X S	44)
RC	TISSUE-Liver;
R PA	Elssonerghis M., Fellower R., Feldmann M., Cheraltock, Y., Submitted (MAY-1995) to the EMPF American Milatahases.
22	-!- FUNCTION: RECEPTOR FOR INF. ALPHA.
88	-1* SUBCREDULAR LOCATION: TYPE I MEMBRANE PROTEIN. 3 JAHUSARO DI GOLLAGAS A DA MORRO HER LOLLO GOLLAGOROGIA NIGORAL
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38	THIS SWINS PROFESTRY IS COPYFIGHT. IT IS PROPOSED THROUGH A COLLABORATION between the SWISS Institute of Bioinformatics—and the EMBE outstation—
88	C the European Midiaformatics (natitute. There are no restrictions on its C use by non-profit institutions as long as its content is in no way

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                          ) (POTENTIAL)
                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 GAGMMAAAMMAAAMMMMMMMMMAAAMAGAAQQQQAQAQQQTQMQTG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 TGTCCCCAAGGAAAAIAIATGCACCTCAAAAIAATGCGATTTGCTGTATA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 AGGATAPGGAATTGPAGGAAGTGTGAGAGGGGTTPPTTPAGGATTGAAAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 AACCACCTCAGACACTGCCTCAGCTGC...TCCAAATGCCGAAAGGAAAT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 CysGlnIleSerGlnGluTyrTyrAspArgLysAlaGlnMetCysCysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 CAAGIGCCAGAAAGGAAACCIAATIGLACAATGACTGTCCAGGCCCGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 aLysCysProProGlyGlnTyrValLysHisPheCys...AsnLysThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 crAspihiValCysAlaAspCysGluAlaSerMetTyrThrGluValTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                              462EAE398C4D6563 CRC64;
                                                                                                                                                                                               Transmembrane: Glycoprotein: Repeats Signal
                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 26.378
                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
N-LINKED (GICNAC.
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                                                                                                                                                                                                                                                                                                   TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                       PROSITE: PS00652; TNFR_NGFR_1: 2. PROSITE: PS50050, INFR_NGFR_2: 3.
                                                                                                                                                 ProDom; PD000771; TNFR_c6; 1.
SMART; $M00208: TNFR: 4.
                                                                                                    HSSP; P19438; INCF;
MGD: MGL:13148R3: Tnfrsflb
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              50319 MW;
                                                       EMBL: M59378; AAA40463.1; -.
EMBL: U39488; AAA85021.1; -.
EMBL: X87128; CAA60618.1; -.
                                            EMBL; M60469; AAA39752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO: TNR2_MOUSE
                                                                                                                                       Ptam; PF00020; INFR_c6; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-525-998A-1 x TNR2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 205.00
Ratio: 1.614
Harity: 50.000
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1119
203
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195
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                                                                                         PIR; B38634; B38634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 AA;
                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                              Receptor,
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                                                                                                                                                                                                          SIGNAL
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01-FEB-1991 (Rel. 17, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
20 AUG-2001 (Rel. 40, Last modition update)
1 FUNOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BENEFICE PROTEIN 2) (TBFL1) (F80) (TNF-RL) (F75) (CD120B) (ETANERGEPT).
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Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
Dower S.K., Cosman D., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A receptor for tumor nectosis factor defines an unusual family of cellular and viral profeins "; Science 248:1019-1023(1990).
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Mammalia, Eutheria, Primates, Catarrilli, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kohno T., Brower M.T., Baker S.L., Schwartz P.E., King M.W.,
Hale K.K., Squires C.H., Thompson P.C., Vannice J.L.;
"A second tumor necrosis factor receptor gene product can shed a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrangserGinprofema 230
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COMMINAL PAPERGRAGIGAA 414
                                                                                      120 laCysGluAlaGlyArgTyrCysAlaLeutysThrHis.....SerGly 134
                                                                                                                                                                                                                                                                                                                                                                                        462 GCACCTCTCCTGCCAGGAGAACACACGCGTGTGC...ACCTGCCATG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 [AlaSerSerArgAlaProAsnClyAsnValLeuCystysAlaCysAlaP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 TAGGITTPTTTTTAAGAAAAAGAGIGIGICICIGIAGIAAAACISAAG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ser Aspthath Ser Ser Thraspvaleysarg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559 AAAAGTTTGGATTGTATGAGTTGTGTGTGTGTGGGAGA TGAAAAGTTAA 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 pAlaValCysAlaProGluScrProThrLeuSerAlalleProArgThrL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 TITICITIGGICITIGGCTTTIAICCCICCICATICATIGGITIAAIGIAI 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703 CGCTACCAACOCTGCAAGTCCAAGCTCTACTCCATTGTTTGTGCAAATC 752
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                                                                                                                                                                                                                                                                                       135 SerCysArgGlnCysMetArgLeuSerLysCysGlyFroGlyFheGlyVa
                                                                                                                                                                                       415 AACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGG...ACCGT
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377 GCIGCAGGAAGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
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APPROXIMATELY 5-FOLID LOWFE AFFINITY FOR THE HETA.

-!- SUMCELLULAR LOCALION: TYPE I MEMBRANE PROTEIN.

-!- FINE PROSPHORYLATED: MAINLY ON SERINE RESIDUES WITH A VERY LOW

-!- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENDREL (IMMUNEX AND
WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOLD
ARTHRITIS (KA). ENBREL CONSIST OF THE EXTRACLILLIAR LIGAND-BINDING
PORTION OF EMPT LINKED TO AN IMMULECHORY. IT BINDS TO

INF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.

-!- SIMILARITY: CONTAINS A LA-WSFP/TNFP-TYPE CYSTEINE-PICH RESIDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Hiochemical properties of the 75 Kba tumor nectosis factor receptor. Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :!- FUNCTION: PECEPTOR FOR TNF-ALPHA HIGH AFFINITY FOR TNA-ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Engelmann H., Novick D., Wallach D., "The control of the human "Two tumor recrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
Brockhaus M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE-93016040; PubMed-1328224;
Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complementary fina elemina of a receptor for tumor mecrosis factor and demonstration of a shed form of the receptor.", Proc. Natl. Avad Sci. H. S.A. 87-6151-6155(1940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park Y.C., Burkitt V., Villa A.K., Tong L., Wu H.; "Structural basis for self-association and receptor recognition of
                                                                                                                                                                                                                                                                                                                                      "Physical mapping and genomic structure of the human TNFR2 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX MEDITUR-99221490; Pubmed-10206649;
                                                                                                                                                                                                             Tensen S T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE: NAME-PROW; NOTE-CD quide CD120b entry;
WAW-Thttp://www.ncbi.olm.nih.grv/prraw/rd/rd170b hrm"
WATABASE: NAME-Enbrot: NOTE-Clinical information on Enbrot;
WWW-Thttp://www.ncbi.olm.fc.nom/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purilication and partial amino acid sequence analysis of two distinct tumor negrosis factor recoptors from HT60 cells.";
J. Hiol. Chem. 265-20131-20138(1940).
                                                                                                                                                                                                    Beltinger C.P., White P.S., Maris T.M., Salman E.P., Tensen
Lepachier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
Brodeur G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heller P.A., Song K., Omasch M.A., Fischer W.H., Chang D.
naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S A 87.8331-8335(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 24-400 65-69: 136-141; 300-406 AND 346-362
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90349572; Pubmed-2166946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 267:21172 21178(1992).
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                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-96299745; PybMcd-9661199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-90110215; PubMed-2153136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDI, INE-91056048; PubMed-2173696;
                                                                                                                                                                                                                                                                                                                                                                              Genomics 35:94-100(3996).
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TUMOR NECROSIS FACTOR RECEPTOR 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 CLGIACOAAGIGCOAFAAAGAAACTIACIIGIALAAIGACIGICTAGGC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation; Pharmacoutical; Abstructure, Signal; SignAL 1 22
                                                                                                                                                                                                                                       EXIRACELLULAR (PTENIIAL)
                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 25.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                114,401
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                                  AACSOCEE 1, JOINED.
AACSOCEE 1, JOINED.
AACSOCEE 1, JOINED.
AACSOCEE 1, JOINED.
                                                                               USD169; AKCEG622.1; JOINED.
USD164; ARCEG622.1; JOINED.
MSS994; AAA36785.1; -.
                                                                                                                                                                                    PROSTIES PSOUSS: INER_NOFE_1: 2.
PROSTIES PSSOUSS: INER_NOFE_2: 4.
PROTECT: 1:ssism.mhyrim.
             AAA63262.1: -.
AAC50622.1: -.
AAC50622.1: JOINED.
                                                                                                                                                                 Pfam: PF00020: INFR_c6: 4.
ProDom: PD000771; TNFR_c6: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 48315 MW;
                                                                                                                                                           InterPro; IPRU01368; INFR_c6.
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US-09-525 998A 1 x TNR2_HUMAN
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                                                                AA:150622.1;
      EMBL; M32315; AAA59929.1;
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1.068
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                                                                                                              A36475; A36475.
A36475; A36475.
B35010; B35010.
                                                                                      US2164; AANBO62
MS5994; AAA3675
                                                                                                                                            PDB: 1CA9; 12-AFR:99.
MIM: 191191; -.
                                                                                                                                     A23666; A23666
                                                                                                      A35356; A35356
                                                                                                                                                                                                                                                                                                                                                                                                                  461 AA;
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ń	styssertlystysserProttytlnHisAlalysValPhetysThrL 69	
224	POGGGGAPAGATAPSSACTESTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
274	PGAGAAAACCACCTCAGACTGCGTGAGGTGCTCCAAATGCGGAAA 320 :: :: :: 	
321 102	GGAAATGGGGTGGGGTGTGTTGTTGGAGGGGGGGGGGG	
371 117	TOTGTGGCTGCAGGAAGAACCASTACCGCATTGGAGIGAAAACCIT 429 ::	
421 129	TTGGAGTGGTTGAATTGGAGGGTGGAGGGGGGGGGGGG	
471 139	CTGCCAGANTAAAATAATATTTTTTTTTTTTTTTTTTTTT	
521 149	TAAGAGAAAAGGGTGTCTCTGTAGTAACTGT 555 ::	
556 166	AAGAAAAOOOOOOOOOOOOOOOOOOOOOOOOOOOO	
592 182	CAGATTGAGAATGTTAAGGGTATGAGGATTTAGGTATTAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	
641 190	TGCCCTGGTCATITICTLIGGTCTITGCCTTTATCCTCTCTTCATT b90 ::	
691 192	GGTTTAATGTTACCAAGGGTGGAAGTCCAAGCTCTACTCCATTGT 740 -	
741 199	TIGIGGGAAAITGAAAAAAAAAAAAAAAAAAAAAAAAAA	
791 206	CTAAGCCCTGGCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC 840 	
841 223	CCCACCTGOSTICASTOCCSTGOCCACIICCACTTCACCTCCAC 887 ::: :::	
888 239	crochaciainacaca	
91 4 256	CCAACTTTGOCGCTCCCGCAAAGAGGGGACACACACCTATCAGGGGGGT 963 	
964	GACCCALCTIGGACACACACACACACACACACACACACACACACACACA	
014 287	TCAGAAGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	

1063 A CONTGGGGACGMUMTANGONDGGAGGAGGT 1097 	1098 GCCCCGFIGCGCIGCAAGGAAFFCGIGCGCGCCCGGGGGCCCCGGGGGCCCGGGGGCCGGGGGG	1148 ACGALLIGATORAPORANIPARANIPARANIPARANIPARIPARIPARIPARIAGE 1194	1195 GCGCAATAGAGATGCTGGGGGCGGGGGGGGGGGGGGGGG	1245 GGCCACGCWGGAGCWGCWGGCCCCCCCCCCACTGCTGCTGC 1294 ::: ::::: :::::	1295 GCTGCCTGGAGGACAT 1310 :		1_documentation_block:	71 (1.2027) 71 (1.40PR-1993 (Rel. 25, Created) 72 (1.40PR-1993 (Rel. 25, Last sequence update) 73 (1.40PR-1994 (Rel. 34, Last annotation update) 75 (1.00FR-1994 (Rel. 34, Last annotation update)	T2. Myxoma virus (strain Lausanne). Viruses; dsDNA viruses, no RNA stage; Poxviridae. Chordoboxvirinae:	Leporipoxvirus. NCBL_TaxID+31530;	SEQUENCE FROM N.A. MEDITINE-91337768 DEDMARG-1651597	upron () March J. () Schreiber M , McFaddon G.; "Myxoma virus expresses a secreted protein with homology to the tumor	<pre>necrosis lador receptor gene lamily that contributes to viral virulence."; virulence."; vir</pre>	-1- FUNCTION: RINDS TO THE AUD HERA, PROBABLY PREVENTS INF TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL.	ANTIVIRAL EFFECTS OF THE CYTOKINE1- SIMILARITY: CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH REGION.	This SWISS PROT entry is appring to it is produced through a collaboration between the collaboration	occurred the while structer of profit matter and the man outstation the the Burpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	RMBL; M95181; AAA49632.1; -, EMBL; A23729; CAA01688.1; -,	PIR; A40565; GQVZML. IISSP; P19489: ITNR INTERPR. IPPO01568; TNFR_C6.	Pfam; PF00020; TNFR_c6; 2. PF00bm; PJU00771; TNFR_c6; 1. SMART: SM00208: TNFR: 3.	<pre>PROSITE: PS00652; TNFR_NGFR_1; 2. PPOSITE: PS50050; TNFR_NGFR_2; 2. Receptor; Glycoprotein: Repeat; Signal.</pre>	SIGNAL 1 16 POTENTIAL. CHAIN 17 326 TOMOR ROCKOUS FACTOR SCLUBLL KLOEPTOR.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 ISerSerThrGluThrCysThrSerSerPheAsnIyrIleSerValGluP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 TOTOCTOCCAGGAGAAGAGAAGAGGTOTOGAGGTOGCATGCAGGTTTC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 heAsnLeuTyrFrcValAsnAspThrSerCysThrThrThrAlaGly... 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 GAAAATATACCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCAC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 GAGATOLOTTOTT99CACASTGAAAOCGGAAAAAA1010F01GGCT047AGGAA 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 TTTCTAAGAGAAAAGGAGTGTGTGTGTGTAGTAACTGTAAGAAAAAGCCT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 GGTCCCICACCIAGGGGACAGGGAGAGAGAGATAIAGTGTGTCCCCAAAG 1 👀
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 ProGlySerTyrAlaSerArgLeuCys...GlyProGlySerAspThrVa 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   40 GIGCICCIGGAGGIGTIGGIGGGAAIAIACGGGGTIATIGGAGT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CysArgGlyA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlutysAspGlyLeurysCysThrSerrysPro 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 lCycSerProCysLysAsnGluThrPheThrAlaSerThrAsnHisAlaP 77
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  4 X TNFR-CYS.
                  TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 2.
TNFR-CYS 4.
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19 AlabroTyrdlyAlaAspArgolyLys
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US-09-525-998A-1 x VT2_MYXVI
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Ratio: 1.695
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Archosouria: Arec: Ne-prathae: Galllioraes, Phanlanidae, Phanlaae;
                                                                                                                                                                                                                                                                                                                        large T.H., Woskamp G., Helder J.C., Madeke M.J., Misku T.P., Shooter E.M., Reichardt L.P.; Shooter E.M., Reichardt L.P.; "Structure and devalepmental expression of the serve growth factor receptor in the chicken central nervous system."; Newcon 2:1123-114(1989).
                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
150W-AFFIRITY REWIT GROWIE PACIOE FEDITIOE ENIGRESIS (NOF ERCEPTOE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOW-AFFINITY NERVE SROWIH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Newlogenesis; Transmembrane; diyeoprotein, Repeat; Phosphorylation; Signal.
567 G......GAGIGCACGARTITGIGHTIACCHTAGA.LCAGAAIGITA 507
                     204 uAcoHisThrAcpTysAsperoValPheHisThrolufyrlyrolyThroluf
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TNFR-CYS 4.
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Pfam, PF00621; INFR_c6, 4.
PFAMIT: SM00005; INFR_1.
PFAMIT: SM00005; INFR_1.
PFAMIT: SM00005; INFR_MSFL1; 3.
PFWSITE: PV50055; INFR_MSFL1; 3.
PWSITE: PV50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                              MEDLINE-90164579; PubMed-2560385;
                                                                                          seq_name. SwindFrot, C.MGFR_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linguistra, INPR_cs
                                           608 AGGGCACTGACGACTCAGGC 527
                                                                 221 erdlySerGlySlyAladly 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Pu/1/4; INGR.
InterPro; IPR000488; Death.
                                                                                                                           STANDARIS
                                                                                                                                                                                                                     Gallus qallus (Chicken).
                                                                                                                                                                                             (CP80-LNGFR) (P75 ICD).
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PIR: A60504; A6:504.
                                                                                                                 seq_documentation_blork:
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                                                                                                                                                                                                                                                                    NCH1_14v10-6031;
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P18519;
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SEP_/THP-PICH. DEATH. BY SIMILARITY. BY SIMILARIT	Length. 48 Gaps: 3 Percent Edontity: 24 92	9 1/1 to: NGFR_CHICK from: 1 to: 416 CTGCCACHODIDGTGCTGGAGGATATACCCCTCAGGGT :::	GTCCCCAAGGAAAATATATCCACCTCAAAATAATTCCATTTGCTGTACC	AAAACCACCTCAGACTGCCTCAGCTCCTCCAAATGCCGAAAGGAAATG 313 alSerAlaThrGluprodysLysProdysThrGlnCysVal GGTCAGCTGTAGATCTTTCTTGGACAGTGGACCGGGACACGTGTG 411 611 612 614 614 615 615 617 617 617 617 617 617 617 617 617 617	AGTGCTICAATTGCAGCTGTGCGTCAATGGGACGTGCAGCTGTGC ercysLysGluCysSerIleCysGluValGlyPheGlyLeuMetFhebro fGCOACGAGAAAAAAAAAAACACCTGTAA ACTGGAGGTTGCAGGTTTGTT fli::::::::::
2346 410 430 49 56 75 75 91 130 130 130 130 130 130 133 133 133 14654	197.50 0.890 45.890 NGFR_CHICK	NGFR_CHICK TGCTCCTGCAG TTLLLLL CULculcul. GTCCCTCACT TLLL LL	AAATATOCACC MALTYE ACGAACCTACTTC ACGAACCTACTTC 111 111 111 1111 1111 WSGIUPTOCYSLA	ACACACHGCC 31UProCyst 31UProCyst 3ATCHCTTCT 1:::1 MGLSCFA!A	10CAGOCTCT 778SerileC ACACAACACC 111:::111
1888 3.33 2.44 3.46 3.46 3.46 1101 1101 1101 1101 1101 1101 1101 11	Scores: Quality Ratio imilarity block:	1/1	PROCCCAAGGA 	AAAACCACCICA ::: Il Seralathra Il Seralathra icactacacacacacacacacacacacacacacacacaca	#GTGCTTCAAT :: ::: erCysLysGlut FGCACCACAA FGCACCACAA FGTAAGASSA TGTAAGAGAA
FT DOMAIN FT DOMAIN FT DISULFID FT CONELICT FT CONELI	ignment ercent. ignment S-09-52	Aliqn seq 31 C 5 V: 81 T ₁	24 Y Y Y Y B S 38 A S 11 C S 1	278 328 328 378 375 499 83 83 83 83 83 83 83 83 83 83 83 83 83	425 A 113 e 472 r 130 c 519 T

146	eSerAspGluAlaAsnPheValAspProCysLeuProCysThr11eCysG	163
557	AGAAAAGCCHGGAGTGCAACAACTTGTGCTTAGCCCAGATTGTT	909
163	luGluAsnGluValMetValLysGluCys	172
607	AAGGGCATTGAGGACTCAGGCACACTGCTGTTGCCTGCTGGTCATTTT	656
173	ThralaThrSerAspAlaGluCysArgAspLeuHisPro	185
657	GOUTITIALOUGTOUTOTTOATTGGTTTAATGTALOG	706
185		185
707	ACCAMOSTOSA A CONTROL O DE COMO DE CAMO DE COMO DE CAMO DE CAM	75
186	AuglipThiThrHisThrProSerLeu	19
757	CCIGAAAAAGAGGGGAAGGTIGAAGGAACIACIAGIAAGCCCIGIGGCCC 11111	806 205
807	AAACCCAAAATTICAATGCAATTOTAAAATTOACOOOTACCTGGGGTT :::	856
857	GTCCCGTGC	- 500
220	 InrValMetGlySerSerGlnProValValSerArqGly	m
886	Ter Ar	925
236	stricturi	253
926	PERCONGRAMMASTACACIACIAN CONTRACA	959
253	alGlyLeuValAlaTyrIleAlaPhoLysArgTrpAsnSerCysLysGin	597
959	GOTGACGCATICCTTGCGAGCCCTCGGCTCCGACGGCATGGGG	1008
34ŭ	AssLysGlnGlyAlaAsnAsnArgProValAsnClnThrProSerProGl	386
1009	CCCCTTCAGA AGTGGGAG GACAGG	1033
286	 couHisSerAspSerGlylleSerValAspSerGlnS	103
1034	CCPACANGCAPARAGECTAGACTATAGECCCGCG	1071 +19
1072	ACCOURTAGGCGTGGAGAAGGTGGGGGGTTGGGC	1110
320	yAspGly	333
1111	TGGAAGG	1117
333	luGluValGluLySLeuheuSerSerSerAlaGluGluThr	350
1118	GTGCGCCCTAGGCTGAGCGACCACAGG ::: ::::::::::::::::::::::::::::::::	1167 363
1168	SCAGAACGGGCGC FGCCFGCGCGAGGCGCAATACAGC	- C
364	(::: ::: ::: CysPheThrArgGluGluSerProAl.	75
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1259	TGCTGGGACGCGTGCGCGGACATGGACTGGCTGCCTGGAGGAC	1308

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Upton C., Delange A.M., Perdden G.; "Itumorigenic paxviruses, are acid of the telomeric region of the Shope libroma virus genome."; Virology 160:20:30(1987).
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form of the INF receptor.";
Hiochem. Biophys. Res. Cermon, 176,335-442(1991).
-i- FUNCTION: BINDS TO INF-ALPHA AND BEIA. PROBABLY PREVENTS INF TO
REACH CELLOLDE AND THEREBY DEAMPENING THE POFENTIAL
ANTIVIRAL EFFECTS OF THE CYTOKINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no KNA stage; Poxviridae: Chordopoxvirinae;
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INFR CYS 3.
INFR CYS 4.
INFR CYS 4.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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Smith C A , Davis I , Wignall <sup>I</sup> M , Din W S , Farrah T , Opton <sup>O</sup>
McPadden G., Goodwin R.G.;
                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Pel. 22, Last sequence update)
15-JUL-1999 (Rel. 28, Last uncutation update)
TUMOR NECHOSIS FACTOR SOLUBLE PROCEPTOR PERCURSOR (PROTEIN T2)
389 laLeuLeuValAlaLeuArgLysIleGlo.....ArgGlyAsp 401
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EMBL; A23727; CAA01687.1; -.
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InterPro; IPROBL368; FNPR_c6.
Plam, PED0020; TNFR_c6; 2.
Problem, ED00771; TNFR_c6; 1.
SMART; SMO0208: TNFR; 3.
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